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SEQUENCE LISTING

<110> BETTER, Marc D.
HORWITZ, Arnold H.

<120> HUMAN ENGINEERED TO ANTIBODIES TO EP-CAM

<130> 117791-072

<140> US 10/816,276

<141> 2004-03-31

<150> US 60/459,334

<151> 2003-03-31

<160> 61

<170> PatentIn version 3.2

<210> 1

<211> 720

<212> DNA

<213> Homo sapiens

<220>

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<223> Mouse Human Chimeric Light Chain DNA and Protein

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Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ala	Ala	Phe	Ser	Asn	Pro	
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Val	Thr	Leu	Gly	Thr	Ser	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	
	15					20				25						
ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aag	192
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
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cca	ggc	cag	tct	cct	cag	ctc	ctg	att	tat	cag	atg	tcc	aac	ctt	gcc	240
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Leu	Ala	
45				50				55							60	
tca	gga	gtc	cca	gac	agg	ttc	agt	agc	agt	ggg	tca	gga	act	gat	ttc	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
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aca	ctg	aga	atc	agc	aga	gtg	gag	gct	gag	gat	gtg	ggt	gtt	tat	tac	336
Thr	Leu	Arg	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
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tgt	gct	caa	aat	cta	gaa	ctt	cct	cgg	acg	ttc	ggt	gga	ggc	acc	aag	384
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	
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ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	432
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	

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145	150	155	160
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac			576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp			
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agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa			624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys			
185	190	195	200
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag			672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln			
205	210	215	220
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 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
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 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
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 Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90
 Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gly Thr Lys
 95 100 105
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cct gga gag aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc	144
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
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aca aaa tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta	192
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu	
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Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly	
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gat gac ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc	288
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tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga	384
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly	
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Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp	
150 155	
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Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu	
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Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser	
175 180 185	
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Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser
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 <223> Low Risk Human Engineered ING-1 Light Chain (LC)

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 15 20 25
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 30 35 40
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 125 130 135 140
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 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 145 150 155
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 160 165 170
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 175 180 185
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NS.txt

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Cys	Ala	Gln 95	Asn	Leu	Glu	Leu	Pro 100	Arg	Thr	Phe	Gly	Gln 105	Gly	Thr	Lys
Leu	Glu 110	Met	Lys	Arg	Thr	Val 115	Ala	Ala	Pro	Ser	Val 120	Phe	Ile	Phe	Pro
Pro 125	Ser	Asp	Glu	Gln	Leu 130	Lys	Ser	Gly	Thr	Ala 135	Ser	Val	Val	Cys	Leu 140
Leu	Asn	Asn	Phe	Tyr 145	Pro	Arg	Glu	Ala	Lys 150	Val	Gln	Trp	Lys	Val 155	Asp
Asn	Ala	Leu	Gln 160	Ser	Gly	Asn	Ser	Gln 165	Glu	Ser	Val	Thr	Glu 170	Gln	Asp
Ser	Lys	Asp 175	Ser	Thr	Tyr	Ser	Leu 180	Ser	Ser	Thr	Leu	Thr 185	Leu	Ser	Lys
Ala	Asp 190	Tyr	Glu	Lys	His	Lys 195	Val	Tyr	Ala	Cys	Glu 200	Val	Thr	His	Gln
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Val	Thr	Pro 15	Gly	Glu	Pro	Gly	Ser 20	Ile	Ser	Cys	Arg	Ser 25	Ser	Lys	Ser	
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Pro	Gly	Gln	Ser	Pro	Gln 50	Leu	Leu	Ile	Tyr	Gln 55	Met	Ser	Asn	Arg	Ala 60	
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Ser	Gly	Val	Pro	Asp 65	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp 75	Phe	
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Cys	Ala	Gln 95	Asn	Leu	Glu	Leu	Pro 100	Arg	Thr	Phe	Gly	Gln 105	Gly	Thr	Lys	

NS.txt																		
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Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp			
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Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp			
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agc	aag	gac	agc	acc	tac	agc	ctc	agc	acc	ctg	acg	ctg	agc	aaa			624	
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys			
			175				180					185						
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag		672	
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln			
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ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag		720	
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205					210					215								

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Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr		
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Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys		
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Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro		
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Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu		
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			160					165					170				
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys		
		175					180					185					
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln		
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Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys			
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 <211> 88
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> KL1 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

 <400> 9
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 atccactgca gacatcgtga tgacccag 88

 <210> 10
 <211> 85
 <212> DNA
 <213> Homo sapiens

 <220>
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 <223> KL2 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

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 tgcagactgg gtcatcacga tgtct 85

 <210> 11
 <211> 88
 <212> DNA
 <213> Homo sapiens

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 <223> KL3 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

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 gcagaaacca gggcagtctc ctcagctg 88

 <210> 12
 <211> 86
 <212> DNA
 <213> Homo sapiens

 <220>
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 <223> KL4 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

 <400> 12
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 <210> 13
 <211> 77
 <212> DNA
 <213> Homo sapiens

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 <223> KL5 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

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 <210> 14
 <211> 75

<212> DNA
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 <223> KL6 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

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 <211> 22
 <212> DNA
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 <220>
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 <223> Low Risk Primers Forward Primer: KF ING-1 Light Chain Oligos

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 <210> 16
 <211> 21
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 <210> 17
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 Light Chain Oligos (Kappa Moderate)

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 gcc caa gca cag atc cag ttg gtg cag tct gga cct gag gtg aag aag 96
 Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
 -1 1 5 10
 cct gga gag tcc gtc aag atc tcc tgc aag gct tct gga tat acc ttc 144
 Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 15 20 25
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 Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt 240
 Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
 50 55 60
 gat gac ttc aag gga cgg ttt acc ttc acc ttg gac acc tct act agc 288
 Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
 65 70 75
 act gcc tat ttg gaa atc tct tct ctc cgg agt gag gac acg gct aca 336
 Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr
 80 85 90
 tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga 384
 Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
 95 100 105
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 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 110 115 120 125
 ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg gcc ctg 480
 Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140
 ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg 528
 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155
 aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta 576
 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 160 165 170
 cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc 624
 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 175 180 185
 agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc 672
 Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 190 195 200 205
 agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa 720
 Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220 225
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 Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 230 235
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 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 240 245 250
 cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac 864
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
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 cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat 912

NS.txt																
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Val	Ser	Val	Thr 305	Val	Val	Leu	His	Asp 310	Trp	Leu	Asn	Gly 315	Lys	Glu		
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Tyr	Lys	Cys 320	Lys	Val	Ser	Asn	Lys 325	Ala	Leu	Pro	Ala	Pro 330	Ile	Glu	Lys	
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Thr	Ile 335	Ser	Lys	Ala	Lys	Gly 340	Gln	Pro	Arg	Glu	Pro 345	Gln	Val	Tyr	Thr	
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Ser	Asn	Gly 385	Gln	Pro	Glu	Asn	Asn	Tyr 390	Lys	Thr	Thr	Pro	Pro 395	Val	Leu	
gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	1296
Asp	Ser	Asp 400	Gly	Ser	Phe	Phe	Leu	Tyr 405	Ser	Lys	Leu	Thr 410	Val	Asp	Lys	
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Lys																

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Pro	Gly -1	Glu	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
Thr	Lys	Tyr	Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Gly	Leu
Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Glu	Glu	Pro	Thr	Tyr	Gly
Asp	Asp	Phe	Lys	Gly	Arg	Phe	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Thr	Ser
Thr	Ala	Tyr	Leu	Glu	Ile	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Thr
Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Ser	Ala	Val	Asp	Tyr	Trp	Gly	Gln	Gly
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu
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NS.txt															
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Thr	Lys	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
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gag	tgg	atg	ggc	tgg	ata	aac	acc	tac	act	gaa	gag	cca	aca	tat	ggt
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cag	aag	ttc	cag	gga	cgg	ttt	acc	ttc	acc	ttg	gac	acc	tct	act	agc
Gln	Lys	Phe	Gln	Gly	Arg	Phe	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Thr	Ser
			65					70					75		
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Thr	Ala	Tyr	Leu	Glu	Ile	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
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Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Ser	Ala	Val	Asp	Tyr	Trp	Gly	Gln	Gly
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Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe
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ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu
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Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp
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Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu
		160					165					170			
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Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser
	175					180					185				
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190					195				200					205	
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Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys
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Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro
			225					230					235		
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Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser
		240					245					250			
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Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp
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Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn
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Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val
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Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu
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Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys
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Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr
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NS.txt																
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Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	
gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	1296
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	
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Ser	Arg	Trp	Gln	Gln	Gly	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu		
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Lys																

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Thr	Lys	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
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Gln	Lys	Phe	Gln	Gly	Arg	Phe	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Thr	Ser
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Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Ser	Ala	Val	Asp	Tyr	Trp	Gly	Gln	Gly
	95					100				105					
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe
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Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu
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Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser
	175					180				185					
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Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys
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Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro
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Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser
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Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp
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Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn

NS.txt

270	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val
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	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys
			320					325					330			
	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr
		335					340					345				
	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr
		350				355					360					365
	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu
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	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu
			385						390					395		
	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys
			400					405					410			
	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu
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	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly
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 <211> 90
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 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> GL2 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
 (gamma low)

<400> 23
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 cttcacctca ggtccagact gcaccaactg 90

<210> 24
 <211> 91
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> GL3 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
 (gamma low)

<400> 24
 tggatatacc ttcacaaaat atggaatgaa ctgggtgaag caggctccag gacagggttt 60
 Page 16

NS.txt 91

aaagtggatg ggctggataa acacctacac t

<210> 25
 <211> 90
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> GL4 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
 (gamma low)

<400> 25
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 ttggctcttc agtgtagggtg tttatccagc 90

<210> 26
 <211> 90
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> GL5 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
 (gamma low)

<400> 26
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 acatatttct gtgcaagatt tggctctgct 90

<210> 27
 <211> 85
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> GL6 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
 (gamma low)

<400> 27
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 gtccacagca gagccaaatc ttgca 85

<210> 28
 <211> 22
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> Human Engineered ING-1 Heavy Chain Oligos-Low Risk Primers
 Forward primer:GF

<400> 28
 ttatgtcgac accatggctt gg 22

<210> 29
 <211> 17
 <212> DNA
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<220>

<221> misc_feature
 <223> Human Engineered ING-1 Heavy Chain Oligos Low Risk Primers
 -Reverse Primer GR

 <220>
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 <223> ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR

 <400> 29
 gaccgatggg ccctttg 17

 <210> 30
 <211> 90
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 <220>
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 <223> GM2 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
 + Moderate Risk Primers

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 cttcacctca gctccagact gcaccaactg 90

 <210> 31
 <211> 91
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <223> GM3 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
 + Moderate Risk Primers

 <400> 31
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 <210> 32
 <211> 90
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <223> GM4 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
 + Moderate Risk Primers

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 ttggctcttc agtgtaggtg tttatccagc 90

 <210> 33
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 <221> misc_feature
 <223> GM5 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
 + Moderate Risk Primers

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<400> 33
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<210> 34
<211> 720
<212> DNA
<213> Homo sapiens

<220>
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<223> P1=P Human Engineered (low risk) ING1 light Chain with one
moderate risk proline change; proline at position 8 (P1)

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<222> (1)..(717)

<220>
<221> mat_peptide
<222> (61)..()

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gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca 96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
-1 1 5 10
gtc act ctg gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt 144
Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Lys Ser
15 20 25
ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa 192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
30 35 40
cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc 240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45 50 55 60
tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc 288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
65 70 75
act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac 336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80 85 90
tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag 384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
95 100 105
ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg 432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
110 115 120
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg 480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125 130 135 140
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat 528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac 576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
160 165 170
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa 624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
175 180 185
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 672

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Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	
	190					195					200					
ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag	720
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys		
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<211> 239
<212> PRT
<213> Homo sapiens
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<400>

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			-1	1				5					10		
Val	Thr	Leu	Gly	Glu	Ser	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser
		15					20					25			
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys
	30					35					40				
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala
45					50					55					60
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe
				65					70					75	
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr
			80					85					90		
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys
		95					100					105			
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
	110					115					120				
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu
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Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
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Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
			160					165					170		
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
		175					180					185			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
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<210> 36
<211> 720
<212> DNA
<213> Homo sapiens
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<220>
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<223> P2=P Human Engineered (low risk) ING1 light Chain with one
moderate risk proline change; proline at position 15 (P2)
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<220>
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<222> (1)..(717)

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<220>
<221> mat_peptide
<222> (61)..()
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Page 20

NS.txt

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Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Ala	Leu	Ser	Asn	Pro	
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gtc	act	cct	gga	gag	tca	ggg	tcc	atc	tcc	tgc	cgg	tct	agt	aag	agt	144
Val	Thr	Pro	Gly	Glu	Ser	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	
		15					20					25				
ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aaa	192
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
		30				35					40					
cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc	240
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala	
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tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
				65				70						75		
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Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
			80					85					90			
tgt	gct	cag	aac	cta	gag	ctt	ccg	cgg	acg	ttc	ggg	cag	ggc	acc	aag	384
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
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Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	
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Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	
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			160					165					170			
agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	624
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	
		175					180					185				
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	672
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	
	190					195					200					
ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag	720
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205					210					215						

<210> 37
 <211> 239
 <212> PRT
 <213> Homo sapiens

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 Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
 15
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 30
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
 45
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 65 70 75

NS.txt

Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr
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		95					100					105			
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
	110					115					120				
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu
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Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
			145						150					155	
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
		160						165					170		
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
		175					180					185			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
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<210> 38
 <211> 720
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> P3=P Human Engineered (low risk) INGI light Chain with one moderate risk proline change; proline at position 18 (P3)

<220>
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 <222> (1)..(717)

<220>
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	Val	Thr	Leu	Gly	Glu	Pro	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	
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	ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aaa	192
	Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
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	Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala	
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	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
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	tgt	gct	cag	aac	cta	gag	ctt	ccg	cgg	acg	ttc	ggg	cag	ggc	acc	aag	384
	Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
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NS.txt																
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Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	
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Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	
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Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	
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Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	
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ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag	720
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys		
205					210					215						

<210> 39
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 <213> Homo sapiens

<400> 39

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Val	Thr	Leu	Gly	Glu	Pro	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser
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Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys
30					35					40					
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala
45					50					55					60
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe
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Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr
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Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys
		95					100					105			
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
						115					120				
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu
125					130					135					140
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
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Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
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Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
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Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> P1P2=Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1) 15(P2)

<220>
 <221> CDS
 <222> (1)..(717)

<220>
 <221> mat_peptide
 <222> (61)..()

<400> 40
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 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
 -20 -15 -10 -5
 gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca 96
 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
 -1 1 5 10
 gtc act cct gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt 144
 Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
 15 20 25
 ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa 192
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 30 35 40
 cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc 240
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
 45 50 55 60
 tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc 288
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac 336
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90
 tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag 384
 Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
 95 100 105
 ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg 432
 Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
 110 115 120
 cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg 480
 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 125 130 135 140
 ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat 528
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 145 150 155
 aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac 576
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 160 165 170
 agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa 624
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 175 180 185
 gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 672
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 190 195 200
 ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 720
 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 205 210 215

<210> 41
 <211> 239
 <212> PRT

<213> Homo sapiens

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<400> 41
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20      -15      -10      -5
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
-1  1  5  10
Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15 20 25
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
30 35 40
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45 50 55 60
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
65 70 75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80 85 90
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
95 100 105
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
110 115 120
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125 130 135 140
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
145 150 155
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
160 165 170
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
175 180 185
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
190 195 200
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210 215

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<210> 42

<211> 720

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> P1P3= Human Engineered (low risk) ING1 light Chain with one
moderate risk proline change; proline at position 8 (P1) 18 (P3)

<220>

<221> CDS

<222> (1)..(717)

<220>

<221> mat_peptide

<222> (61)..()

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<400> 42
atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct      48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20      -15      -10      -5
gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca      96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
-1  1  5  10
gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt      144
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15 20 25
ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192

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NS.txt																
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
30	30					35				40						
cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc	240
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala	
45					50					55					60	
tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
				65					70					75		
act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	gtt	tat	tac	336
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
			80					85					90			
tgt	gct	cag	aac	cta	gag	ctt	ccg	cgg	acg	ttc	ggt	cag	ggc	acc	aag	384
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
		95					100					105				
ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	432
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	
	110					115					120					
cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	480
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	
					130					135					140	
ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	528
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	
				145				150						155		
aac	gcc	ctc	caa	tcg	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	576
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	
			160					165					170			
agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	624
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	
		175					180				185					
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	672
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	
	190					195					200					
ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag	720
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys		
	205				210					215						

<210> 43
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 43
 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
 -20 -15 -10 -5
 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
 -1 1
 Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Lys Ser
 15 20 25
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 30 35 40
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90
 Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
 95 100 105
 Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
 110 115 120
 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 125 130 135 140
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp

NS.txt

Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
			160					165					170		
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
		175					180					185			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
	190					195					200				
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
205					210					215					

<210> 44
 <211> 720
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> P2P3=Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1) 18 (P3)

<220>
 <221> CDS
 <222> (1)..(717)

<220>
 <221> mat_peptide
 <222> (61)..()

<400> 44	atg	agg	ttc	tct	gct	cag	ctt	ctg	ggg	ctg	ctt	gtg	ctc	tgg	atc	cct	48
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	-20				-15				-10							-5	
	gga	tcc	act	gca	gac	atc	gtg	atg	acc	cag	tct	gca	ctc	tcc	aat	cca	96
	Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Ala	Leu	Ser	Asn	Pro	
			-1	1				5					10				
	gtc	act	cct	gga	gag	ccg	ggt	tcc	atc	tcc	tgc	cgg	tct	agt	aag	agt	144
	Val	Thr	Pro	Gly	Glu	Pro	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	
			15				20					25					
	ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aaa	192
	Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
			30			35					40						
	cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc	240
	Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala	
	45					50					55					60	
	tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc	288
	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
					65				70						75		
	act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	gtt	tat	tac	336
	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
				80					85					90			
	tgt	gct	cag	aac	cta	gag	ctt	ccg	cgg	acg	ttc	ggt	cag	ggc	acc	aag	384
	Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
			95					100					105				
	ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	432
	Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	
			110				115					120					
	cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	480
	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	
	125					130					135					140	
	ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	528
	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	
					145					150					155		
	aac	gcc	ctc	caa	tcg	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	576

									NS.txt									
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp			
			160					165					170					
agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa			624
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys			
		175					180					185						
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag			672
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln			
	190					195					200							
ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag			720
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
205					210					215								

<210> 45
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 45
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 -20 -15 -10 -5
 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
 -1 1 5 10
 Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
 15 20 25
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 30 35 40
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90
 Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
 95 100 105
 Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
 110 115 120
 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 125 130 135 140
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 145 150 155
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 160 165 170
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 175 180 185
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 190 195 200
 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 205 210 215

<210> 46
 <211> 85
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> P1 Oligo Human Engineered ING-1 with proline oligos

<400> 46	actcttacta gaccggcagg agatggaacc tgactctccc agagtgactg gattggagag	60
	tggagactgg gtcatcacga tgtct	85

<210> 47

<211> 85
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <223> P2 Oligo Human Engineered ING-1 with proline oligos

 <400> 47
 actcttacta gaccggcagg agatggaacc tgactctcca ggagtgactg gattggagag 60
 tgcagactgg gtcatcacga tgtct 85

 <210> 48
 <211> 85
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <223> P3 Oligo Human Engineered ING-1 with proline oligos

 <400> 48
 actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag 60
 tgcagactgg gtcatcacga tgtct 85

 <210> 49
 <211> 85
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <223> P1P2 Oligo Human Engineered ING-1 with proline oligos

 <400> 49
 actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gattggagag 60
 tgcagactgg gtcatcacga tgtct 85

 <210> 50
 <211> 85
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <223> P1P3 Oligo Human Engineered ING-1 with proline oligos

 <400> 50
 actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag 60
 tggagactgg gtcatcacga tgtct 85

 <210> 51
 <211> 85
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <223> P2P3 Oligo Human Engineered ING-1 with proline oligos

 <400> 51
 actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gattggagag 60
 tgcagactgg gtcatcacga tgtct 85

<210> 52
 <211> 19
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Reverse Primer KBsr ING-1 Light Chain

<400> 52
 cttactagac cggcaggag

19

<210> 53
 <211> 798
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> EpCam truncated sequence

<220>
 <221> CDS
 <222> (1)..(795)

<400> 53
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 Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
 1 5 10 15
 acg gcg act ttt gcc gca gct cag gaa gaa tgt gtc tgt gaa aac tac 96
 Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
 20 25 30
 aag ctg gcc gta aac tgc ttt gtg aat aat aat cgt caa tgc cag tgt 144
 Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
 35 40 45
 act tca gtt ggt gca caa aat gtc att tgc tca aag ctg gct gcc 192
 Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
 50 55 60
 aaa tgt ttg gtg atg aag gca gaa atg aat ggc tca aaa ctt ggg aga 240
 Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
 65 70 75 80
 aga gca aaa cct gaa ggg gcc ctc cag aac aat gat ggg ctt tat gat 288
 Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
 85 90 95
 cct gac tgc gat gag agc ggg ctc ttt aag gcc aag cag tgc aac ggc 336
 Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
 100 105 110
 acc tcc acg tgc tgg tgt gtg aac act gct ggg gtc aga aga aca gac 384
 Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
 115 120 125
 aag gac act gaa ata acc tgc tct gag cga gtg aga acc tac tgg atc 432
 Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
 130 135 140
 atc att gaa cta aaa cac aaa gca aga gaa aaa cct tat gat agt aaa 480
 Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
 145 150 155 160
 agt ttg cgg act gca ctt cag aag gag atc aca acg cgt tat caa ctg 528
 Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
 165 170 175
 gat cca aaa ttt atc acg agt att ttg tat gag aat aat gtt atc act 576
 Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
 180 185 190

									NS.txt										
att	gat	ctg	gtt	caa	aat	tct	tct	caa	aaa	act	cag	aat	gat	gtg	gac				624
Ile	Asp	Leu	Val	Gln	Asn	Ser	Ser	Gln	Lys	Thr	Gln	Asn	Asp	Val	Asp				
		195					200					205							
ata	gct	gat	gtg	gct	tat	tat	ttt	gaa	aaa	gat	gtt	aaa	ggg	gaa	tcc				672
Ile	Ala	Asp	Val	Ala	Tyr	Tyr	Phe	Glu	Lys	Asp	Val	Lys	Gly	Glu	Ser				
	210					215					220								
ttg	ttt	cat	tct	aag	aaa	atg	gac	ctg	aca	gta	aat	ggg	gaa	caa	ctg				720
Leu	Phe	His	Ser	Lys	Lys	Met	Asp	Leu	Thr	Val	Asn	Gly	Glu	Gln	Leu				
	225				230					235					240				
gat	ctg	gat	cct	ggg	caa	act	tta	att	tat	tat	gtt	gat	gaa	aaa	gca				768
Asp	Leu	Asp	Pro	Gly	Gln	Thr	Leu	Ile	Tyr	Tyr	Val	Asp	Glu	Lys	Ala				
				245				250						255					
cct	gaa	ttc	tca	atg	cag	ggg	cta	aaa	taa										798
Pro	Glu	Phe	Ser	Met	Gln	Gly	Leu	Lys											
			260					265											

<210> 54
 <211> 265
 <212> PRT
 <213> Homo sapiens

<400> 54

Met	Ala	Pro	Pro	Gln	Val	Leu	Ala	Phe	Gly	Leu	Leu	Leu	Ala	Ala	Ala
1				5					10					15	
Thr	Ala	Thr	Phe	Ala	Ala	Ala	Gln	Glu	Glu	Cys	Val	Cys	Glu	Asn	Tyr
			20					25					30		
Lys	Leu	Ala	Val	Asn	Cys	Phe	Val	Asn	Asn	Asn	Arg	Gln	Cys	Gln	Cys
		35				40						45			
Thr	Ser	Val	Gly	Ala	Gln	Asn	Thr	Val	Ile	Cys	Ser	Lys	Leu	Ala	Ala
	50					55					60				
Lys	Cys	Leu	Val	Met	Lys	Ala	Glu	Met	Asn	Gly	Ser	Lys	Leu	Gly	Arg
65				70						75					80
Arg	Ala	Lys	Pro	Glu	Gly	Ala	Leu	Gln	Asn	Asn	Asp	Gly	Leu	Tyr	Asp
			85						90					95	
Pro	Asp	Cys	Asp	Glu	Ser	Gly	Leu	Phe	Lys	Ala	Lys	Gln	Cys	Asn	Gly
			100					105					110		
Thr	Ser	Thr	Cys	Trp	Cys	Val	Asn	Thr	Ala	Gly	Val	Arg	Arg	Thr	Asp
		115					120					125			
Lys	Asp	Thr	Glu	Ile	Thr	Cys	Ser	Glu	Arg	Val	Arg	Thr	Tyr	Trp	Ile
	130					135					140				
Ile	Ile	Glu	Leu	Lys	His	Lys	Ala	Arg	Glu	Lys	Pro	Tyr	Asp	Ser	Lys
145					150					155					160
Ser	Leu	Arg	Thr	Ala	Leu	Gln	Lys	Glu	Ile	Thr	Thr	Arg	Tyr	Gln	Leu
				165					170					175	
Asp	Pro	Lys	Phe	Ile	Thr	Ser	Ile	Leu	Tyr	Glu	Asn	Asn	Val	Ile	Thr
			180					185					190		
Ile	Asp	Leu	Val	Gln	Asn	Ser	Ser	Gln	Lys	Thr	Gln	Asn	Asp	Val	Asp
		195					200					205			
Ile	Ala	Asp	Val	Ala	Tyr	Tyr	Phe	Glu	Lys	Asp	Val	Lys	Gly	Glu	Ser
	210					215					220				
Leu	Phe	His	Ser	Lys	Lys	Met	Asp	Leu	Thr	Val	Asn	Gly	Glu	Gln	Leu
225					230					235					240
Asp	Leu	Asp	Pro	Gly	Gln	Thr	Leu	Ile	Tyr	Tyr	Val	Asp	Glu	Lys	Ala
				245					250					255	
Pro	Glu	Phe	Ser	Met	Gln	Gly	Leu	Lys							
			260					265							

<210> 55
 <211> 945
 <212> DNA
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<220>

<221> misc_feature

<223> Full-Length EpCam

<220>

<221> CDS

<222> (1)..(942)

<220>

<221> mat_peptide

<222> (70)..()

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      Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
      -20 -15 -10
      acg gcg act ttt gcc gca gct cag gaa gaa tgt gtc tgt gaa aac tac      96
      Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
      -5 1
      aag ctg gcc gta aac tgc ttt gtg aat aat aat cgt caa tgc cag tgt      144
      Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
      10 15 20 25
      act tca gtt ggt gca caa aat act gtc att tgc tca aag ctg gct gcc      192
      Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
      30 40
      aaa tgt ttg gtg atg aag gca gaa atg aat ggc tca aaa ctt ggg aga      240
      Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
      45 50 55
      aga gca aaa cct gaa ggg gcc ctc cag aac aat gat ggg ctt tat gat      288
      Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
      60 65 70
      cct gac tgc gat gag agc ggg ctc ttt aag gcc aag cag tgc aac ggc      336
      Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
      75 80 85
      acc tcc acg tgc tgg tgt gtg aac act gct ggg gtc aga aga aca gac      384
      Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
      90 95 100 105
      aag gac act gaa ata acc tgc tct gag cga gtg aga acc tac tgg atc      432
      Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
      110 115 120
      atc att gaa cta aaa cac aaa gca aga gaa aaa cct tat gat agt aaa      480
      Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
      125 130 135
      agt ttg cgg act gca ctt cag aag gag atc aca acg cgt tat caa ctg      528
      Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
      140 145 150
      gat cca aaa ttt atc acg agt att ttg tat gag aat aat gtt atc act      576
      Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
      155 160 165
      att gat ctg gtt caa aat tct tct caa aaa act cag aat gat gtg gac      624
      Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
      170 175 180 185
      ata gct gat gtg gct tat tat ttt gaa aaa gat gtt aaa ggt gaa tcc      672
      Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
      190 195 200
      ttg ttt cat tct aag aaa atg gac ctg aca gta aat ggg gaa caa ctg      720
      Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
      205 210 215
      gat ctg gat cct ggt caa act tta att tat tat gtt gat gaa aaa gca      768
      Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
      220 225 230
      cct gaa ttc tca atg cag ggt cta aaa gct ggt gtt att gct gtt att      816
      Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
      235 240 245

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gtg	gtt	gtg	gtg	ata	gca	gtt	gtt	gct	gga	att	gtt	gtg	ctg	gtt	att				864
Val	Val	Val	Val	Ile	Ala	Val	Val	Ala	Gly	Ile	Val	Val	Leu	Val	Ile				
250					255				260						265				
tcc	aga	aag	aag	aga	atg	gca	aag	tat	gag	aag	gct	gag	ata	aag	gag				912
Ser	Arg	Lys	Lys	Arg	Met	Ala	Lys	Tyr	Glu	Lys	Ala	Glu	Ile	Lys	Glu				
				270					275					280					
atg	ggt	gag	atg	cat	agg	gaa	ctc	aat	gca	taa									945
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 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 56

Met	Ala	Pro	Pro	Gln	Val	Leu	Ala	Phe	Gly	Leu	Leu	Leu	Ala	Ala	Ala
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Thr	Ala	Thr	Phe	Ala	Ala	Ala	Gln	Glu	Glu	Cys	Val	Cys	Glu	Asn	Tyr
		-5				-1	1				5				
Lys	Leu	Ala	Val	Asn	Cys	Phe	Val	Asn	Asn	Asn	Arg	Gln	Cys	Gln	Cys
10				15					20					25	
Thr	Ser	Val	Gly	Ala	Gln	Asn	Thr	Val	Ile	Cys	Ser	Lys	Leu	Ala	Ala
				30				35					40		
Lys	Cys	Leu	Val	Met	Lys	Ala	Glu	Met	Asn	Gly	Ser	Lys	Leu	Gly	Arg
			45					50					55		
Arg	Ala	Lys	Pro	Glu	Gly	Ala	Leu	Gln	Asn	Asn	Asp	Gly	Leu	Tyr	Asp
		60					65				70				
Pro	Asp	Cys	Asp	Glu	Ser	Gly	Leu	Phe	Lys	Ala	Lys	Gln	Cys	Asn	Gly
	75					80					85				
Thr	Ser	Thr	Cys	Trp	Cys	Val	Asn	Thr	Ala	Gly	Val	Arg	Arg	Thr	Asp
90				95						100					105
Lys	Asp	Thr	Glu	Ile	Thr	Cys	Ser	Glu	Arg	Val	Arg	Thr	Tyr	Trp	Ile
				110					115					120	
Ile	Ile	Glu	Leu	Lys	His	Lys	Ala	Arg	Glu	Lys	Pro	Tyr	Asp	Ser	Lys
			125					130					135		
Ser	Leu	Arg	Thr	Ala	Leu	Gln	Lys	Glu	Ile	Thr	Thr	Arg	Tyr	Gln	Leu
		140					145					150			
Asp	Pro	Lys	Phe	Ile	Thr	Ser	Ile	Leu	Tyr	Glu	Asn	Asn	Val	Ile	Thr
	155					160					165				
Ile	Asp	Leu	Val	Gln	Asn	Ser	Ser	Gln	Lys	Thr	Gln	Asn	Asp	Val	Asp
170				175						180					185
Ile	Ala	Asp	Val	Ala	Tyr	Tyr	Phe	Glu	Lys	Asp	Val	Lys	Gly	Glu	Ser
				190				195						200	
Leu	Phe	His	Ser	Lys	Lys	Met	Asp	Leu	Thr	Val	Asn	Gly	Glu	Gln	Leu
			205					210					215		
Asp	Leu	Asp	Pro	Gly	Gln	Thr	Leu	Ile	Tyr	Tyr	Val	Asp	Glu	Lys	Ala
		220					225					230			
Pro	Glu	Phe	Ser	Met	Gln	Gly	Leu	Lys	Ala	Gly	Val	Ile	Ala	Val	Ile
	235					240					245				
Val	Val	Val	Val	Ile	Ala	Val	Val	Ala	Gly	Ile	Val	Val	Leu	Val	Ile
250				255						260					265
Ser	Arg	Lys	Lys	Arg	Met	Ala	Lys	Tyr	Glu	Lys	Ala	Glu	Ile	Lys	Glu
				270					275					280	
Met	Gly	Glu	Met	His	Arg	Glu	Leu	Asn	Ala						
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<210> 57
 <211> 26
 <212> DNA
 <213> Homo sapiens

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<221> misc_feature
<223> Forward Primer (for both soluble and full length Ep-CAM): EC-1

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26

<210> 58
<211> 31
<212> DNA
<213> Homo sapiens

<220>
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<223> Ep-CAM Reverse Primer (for soluble Ep-CAM): EC-2

<400> 58
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31

<210> 59
<211> 30
<212> DNA
<213> Homo sapiens

<220>
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<223> Ep-CAM Reverse Primer (for full-length Ep-CAM): EC-3

<400> 59
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30

<210> 60
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<212> PRT
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<220>
<221> MISC_FEATURE
<223> Variable Region for Mouse-Human Chimeric ING-1 Light Chain

<400> 60

Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro Val Thr Leu Gly
1           5           10           15

Thr Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20           25           30

Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35           40           45

Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala Ser Gly Val Pro
50           55           60

Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile
65           70           75           80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ala Gln Asn

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85

90

95

Leu Glu Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Met Lys
 100 105 110

<210> 61
 <211> 116
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> Variable Region for Mouse-Human Chimeric ING-1 Heavy Chain
 <400> 61

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Tyr
 20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45

Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly Asp Asp Phe
 50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Asn
 65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Thr Ala Thr Tyr Phe Cys
 85 90 95

Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly Thr Ser Val
 100 105 110

Thr Val Ser Ser
 115